

AMERICA

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NOV 13 2001

TECH CENTER 1600/2900

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/545,334B

DATE: 07/26/2001

TIME: 10:33:53

Input Set : A:\0803.SEQLIST.txt

Output Set: N:\CRF3\07262001\I545334B.raw

#9/K.T.
11-15-01

RAW SEQ
Listing

ENTERED

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4 <110> APPLICANT: Zinselmeier, Chris
5     Habben, Jeff
6     Tomes, Dwight
8 <120> TITLE OF INVENTION: Regulated Expression of Genes in Plant
9     Seeds
11 <130> FILE REFERENCE: 0803
13 <140> CURRENT APPLICATION NUMBER: US 09/545,334B
14 <141> CURRENT FILING DATE: 2000-04-07
16 <150> PRIOR APPLICATION NUMBER: US 60/129,844
17 <151> PRIOR FILING DATE: 1999-04-16
19 <160> NUMBER OF SEQ ID NOS: 12
22 <170> SOFTWARE: FastSEQ for Windows Version 3.0
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 1608
27 <212> TYPE: DNA
28 <213> ORGANISM: Zea mays
30 <220> FEATURE:
31 <221> NAME/KEY: CDS
32 <222> LOCATION: (1)...(1605)
34 <400> SEQUENCE: 1
35 atg gcg gtg gtt tat tac ctg ctg ctg gcc ggg ctg atc gcc tgc tct      48
36 Met Ala Val Val Tyr Leu Leu Leu Ala Gly Leu Ile Ala Cys Ser
37 1 5 10 15
39 cat gca cta gcg gca ggc acg ctt gcg ctc gga gaa gat cgc ggc cgt      96
40 His Ala Leu Ala Ala Gly Thr Leu Ala Leu Gly Glu Asp Arg Gly Arg
41 20 25 30
43 ccc tgg cca gcc ttc ctc gcc gcg ctg gcc ttg gac ggc aag ctc cgg      144
44 Pro Trp Pro Ala Phe Leu Ala Ala Leu Ala Leu Asp Gly Lys Leu Arg
45 35 40 45
47 acc gac agc aac gcg acg gcg gcg gcc tcg acg gac ttc ggc aac atc      192
48 Thr Asp Ser Asn Ala Thr Ala Ala Ala Ser Thr Asp Phe Gly Asn Ile
49 50 55 60
51 acg tcg gcg ctc ccg gcg gcg gtc cta tac ccg tcg tcc acg ggc gac      240
52 Thr Ser Ala Leu Pro Ala Ala Val Leu Tyr Pro Ser Ser Thr Gly Asp
53 65 70 75 80
55 ctg gtg gcg ctg ctg agc gcg gcc aac tcc acc ccg ggg tgg ccc tac      288
56 Leu Val Ala Leu Leu Ser Ala Ala Asn Ser Thr Pro Gly Trp Pro Tyr
57 85 90 95
59 acc atc gcg ttc cgc ggc cgc gcc cac tcc ctc atg ggc cag gcc ttc      336
60 Thr Ile Ala Phe Arg Gly Arg Gly His Ser Leu Met Gly Gln Ala Phe
61 100 105 110
63 gcc ccc ggc ggg gtg gtc gtc aac atg gcg tcc ctg ggc gac gcc gcc      384
64 Ala Pro Gly Gly Val Val Val Asn Met Ala Ser Leu Gly Asp Ala Ala
65 115 120 125
67 gcc gcc gcg ccg ccg cgc gtc aac gtg tcc gcg gac ggc cgc tac gtg      432
68 Ala Ala Ala Pro Pro Arg Val Asn Val Ser Ala Asp Gly Arg Tyr Val
69 130 135 140

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71	gac gcc ggc ggc gag cag gtg tgg atc gac gtg ctg cgc gcg tct ctg	480
72	Asp Ala Gly Gly Glu Gln Val Trp Ile Asp Val Leu Arg Ala Ser Leu	
73	145 150 155 160	
75	gcg cgc ggc gtg gcg ccg cgc tcc tgg acc gac tac ctc tac ctc acc	528
76	Ala Arg Gly Val Ala Pro Arg Ser Trp Thr Asp Tyr Leu Tyr Leu Thr	
77	165 170 175	
79	gtc ggc ggc acg ctg tcc aac gca ggc atc agc ggc cag gcg ttc cgc	576
80	Val Gly Gly Thr Leu Ser Asn Ala Gly Ile Ser Gly Gln Ala Phe Arg	
81	180 185 190	
83	cac ggc cca cag ata tct aac gtg ctg gag atg gac gtt atc acc ggc	624
84	His Gly Pro Gln Ile Ser Asn Val Leu Glu Met Asp Val Ile Thr Gly	
85	195 200 205	
87	cat ggg gag atg gtg acg tgc tcc aag cag ctg aac gcg gac ctg ttc	672
88	His Gly Glu Met Val Thr Cys Ser Lys Gln Leu Asn Ala Asp Leu Phe	
89	210 215 220	
91	gac gcc gtc ctg ggc ggg ctg ggg cag ttc gga gtg atc acc cgg gcc	720
92	Asp Ala Val Leu Gly Gly Leu Gly Gln Phe Gly Val Ile Thr Arg Ala	
93	225 230 235 240	
95	cgg atc gcg gtg gag ccg gcg ccg gcg cgg gcg cgg tgg gtg cgg ctc	768
96	Arg Ile Ala Val Glu Pro Ala Pro Ala Arg Ala Arg Trp Val Arg Leu	
97	245 250 255	
99	gtg tac acc gac ttc gcg gcg ttc agc gcc gac cag gag cgg ctg acc	816
100	Val Tyr Thr Asp Phe Ala Ala Phe Ser Ala Asp Gln Glu Arg Leu Thr	
101	260 265 270	
103	gcc ccg cgg ccc ggc ggc ggc ggc gcg tcg ttc ggc ccg atg agc tac	864
104	Ala Pro Arg Pro Gly Gly Gly Gly Ala Ser Phe Gly Pro Met Ser Tyr	
105	275 280 285	
107	gtg gaa ggg tcg gtg ttc gtg aac cag agc ctg gcg acc gac ctg gcg	912
108	Val Glu Gly Ser Val Phe Val Asn Gln Ser Leu Ala Thr Asp Leu Ala	
109	290 295 300	
111	aac acg ggg ttc ttc acc gac gcc gac gtc gcc cgg atc gtc gcg ctc	960
112	Asn Thr Gly Phe Phe Thr Asp Ala Asp Val Ala Arg Ile Val Ala Leu	
113	305 310 315 320	
115	gcc ggg gag cgg aac gcc acc acc gtg tac agc atc gag gcc acg ctc	1008
116	Ala Gly Glu Arg Asn Ala Thr Thr Val Tyr Ser Ile Glu Ala Thr Leu	
117	325 330 335	
119	aac tac gac aac gcc acg gcg gcg gcg gcg gtg gac cag gag ctc gcg	1056
120	Asn Tyr Asp Asn Ala Thr Ala Ala Ala Val Asp Gln Glu Leu Ala	
121	340 345 350	
123	tcc gtg ctg ggc acg ctg agc tac gtg gaa ggg ttc gcg ttc cag cgc	1104
124	Ser Val Leu Gly Thr Leu Ser Tyr Val Glu Gly Phe Ala Phe Gln Arg	
125	355 360 365	
127	gac gtg tcc tac acg gcg ttc ctt gac cgg gtg cac ggc gag gag gtg	1152
128	Asp Val Ser Tyr Thr Ala Phe Leu Asp Arg Val His Gly Glu Glu Val	
129	370 375 380	
131	gcg ctc aac aag ctg ggg ctg tgg cgg gtg ccg cac ccg tgg ctc aac	1200
132	Ala Leu Asn Lys Leu Gly Leu Trp Arg Val Pro His Pro Trp Leu Asn	
133	385 390 395 400	
135	atg ttc gtg ccg cgc tcg cgc atc gcc gac ttc gac cgc ggc gtc ttc	1248

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136 Met Phe Val Pro Arg Ser Arg Ile Ala Asp Phe Asp Arg Gly Val Phe
137          405          410          415
139 aag ggc atc ttg cag ggc acc gac atc gtc ggc ccg ctc atc gtc tac      1296
140 Lys Gly Ile Leu Gln Gly Thr Asp Ile Val Gly Pro Leu Ile Val Tyr
141          420          425          430
143 ccc ctc aac aaa tcc atg tgg gac gac ggc atg tcg gcg gcg acg ccg      1344
144 Pro Leu Asn Lys Ser Met Trp Asp Asp Gly Met Ser Ala Ala Thr Pro
145          435          440          445
147 tcg gag gac gtg ttc tac gcg gtg tcg ctg ctc ttc tcg tcg gtg gcg      1392
148 Ser Glu Asp Val Phe Tyr Ala Val Ser Leu Leu Phe Ser Ser Val Ala
149          450          455          460
151 ccc aac gac ctg gcg agg ctg cag gag cag aac agg agg atc ctg cgc      1440
152 Pro Asn Asp Leu Ala Arg Leu Gln Glu Gln Asn Arg Arg Ile Leu Arg
153          465          470          475          480
155 ttc tgc gac ctc gcc ggg atc cag tac aag acc tac ctg gcg cgg cac      1488
156 Phe Cys Asp Leu Ala Gly Ile Gln Tyr Lys Thr Tyr Leu Ala Arg His
157          485          490          495
159 acg gac cgc agt gac tgg gtc cgc cac ttc ggc gcc gcc gag tgg aat      1536
160 Thr Asp Arg Ser Asp Trp Val Arg His Phe Gly Ala Ala Glu Trp Asn
161          500          505          510
163 cgc ttc gtg gag atg aag aac aag tac gac ccc aag agg ctg ctc tcc      1584
164 Arg Phe Val Glu Met Lys Asn Lys Tyr Asp Pro Lys Arg Leu Leu Ser
165          515          520          525
167 ccc ggc cag gac atc ttc aac tga      1608
168 Pro Gly Gln Asp Ile Phe Asn
169          530          535
172 <210> SEQ ID NO: 2
173 <211> LENGTH: 535
174 <212> TYPE: PRT
175 <213> ORGANISM: Zea mays
177 <400> SEQUENCE: 2
178 Met Ala Val Val Tyr Tyr Leu Leu Leu Ala Gly Leu Ile Ala Cys Ser
179 1          5          10          15
180 His Ala Leu Ala Ala Gly Thr Leu Ala Leu Gly Glu Asp Arg Gly Arg
181          20          25          30
182 Pro Trp Pro Ala Phe Leu Ala Ala Leu Ala Leu Asp Gly Lys Leu Arg
183          35          40          45
184 Thr Asp Ser Asn Ala Thr Ala Ala Ala Ser Thr Asp Phe Gly Asn Ile
185          50          55          60
186 Thr Ser Ala Leu Pro Ala Ala Val Leu Tyr Pro Ser Ser Thr Gly Asp
187          65          70          75          80
188 Leu Val Ala Leu Leu Ser Ala Ala Asn Ser Thr Pro Gly Trp Pro Tyr
189          85          90          95
190 Thr Ile Ala Phe Arg Gly Arg Gly His Ser Leu Met Gly Gln Ala Phe
191          100          105          110
192 Ala Pro Gly Gly Val Val Val Asn Met Ala Ser Leu Gly Asp Ala Ala
193          115          120          125
194 Ala Ala Ala Pro Pro Arg Val Asn Val Ser Ala Asp Gly Arg Tyr Val
195          130          135          140

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196 Asp Ala Gly Gly Glu Gln Val Trp Ile Asp Val Leu Arg Ala Ser Leu
197 145 150 155 160
198 Ala Arg Gly Val Ala Pro Arg Ser Trp Thr Asp Tyr Leu Tyr Leu Thr
199 165 170 175
200 Val Gly Gly Thr Leu Ser Asn Ala Gly Ile Ser Gly Gln Ala Phe Arg
201 180 185 190
202 His Gly Pro Gln Ile Ser Asn Val Leu Glu Met Asp Val Ile Thr Gly
203 195 200 205
204 His Gly Glu Met Val Thr Cys Ser Lys Gln Leu Asn Ala Asp Leu Phe
205 210 215 220
206 Asp Ala Val Leu Gly Gly Leu Gly Gln Phe Gly Val Ile Thr Arg Ala
207 225 230 235 240
208 Arg Ile Ala Val Glu Pro Ala Pro Ala Arg Ala Arg Trp Val Arg Leu
209 245 250 255
210 Val Tyr Thr Asp Phe Ala Ala Phe Ser Ala Asp Gln Glu Arg Leu Thr
211 260 265 270
212 Ala Pro Arg Pro Gly Gly Gly Gly Ala Ser Phe Gly Pro Met Ser Tyr
213 275 280 285
214 Val Glu Gly Ser Val Phe Val Asn Gln Ser Leu Ala Thr Asp Leu Ala
215 290 295 300
216 Asn Thr Gly Phe Phe Thr Asp Ala Asp Val Ala Arg Ile Val Ala Leu
217 305 310 315 320
218 Ala Gly Glu Arg Asn Ala Thr Thr Val Tyr Ser Ile Glu Ala Thr Leu
219 325 330 335
220 Asn Tyr Asp Asn Ala Thr Ala Ala Ala Ala Val Asp Gln Glu Leu Ala
221 340 345 350
222 Ser Val Leu Gly Thr Leu Ser Tyr Val Glu Gly Phe Ala Phe Gln Arg
223 355 360 365
224 Asp Val Ser Tyr Thr Ala Phe Leu Asp Arg Val His Gly Glu Glu Val
225 370 375 380
226 Ala Leu Asn Lys Leu Gly Leu Trp Arg Val Pro His Pro Trp Leu Asn
227 385 390 395 400
228 Met Phe Val Pro Arg Ser Arg Ile Ala Asp Phe Asp Arg Gly Val Phe
229 405 410 415
230 Lys Gly Ile Leu Gln Gly Thr Asp Ile Val Gly Pro Leu Ile Val Tyr
231 420 425 430
232 Pro Leu Asn Lys Ser Met Trp Asp Asp Gly Met Ser Ala Ala Thr Pro
233 435 440 445
234 Ser Glu Asp Val Phe Tyr Ala Val Ser Leu Leu Phe Ser Ser Val Ala
235 450 455 460
236 Pro Asn Asp Leu Ala Arg Leu Gln Glu Gln Asn Arg Arg Ile Leu Arg
237 465 470 475 480
238 Phe Cys Asp Leu Ala Gly Ile Gln Tyr Lys Thr Tyr Leu Ala Arg His
239 485 490 495
240 Thr Asp Arg Ser Asp Trp Val Arg His Phe Gly Ala Ala Glu Trp Asn
241 500 505 510
242 Arg Phe Val Glu Met Lys Asn Lys Tyr Asp Pro Lys Arg Leu Leu Ser
243 515 520 525
244 Pro Gly Gln Asp Ile Phe Asn

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245          530          535
247 <210> SEQ ID NO: 3
248 <211> LENGTH: 51
249 <212> TYPE: DNA
250 <213> ORGANISM: Artificial Sequence
252 <220> FEATURE:
253 <223> OTHER INFORMATION: Synthesized based on sequence from Agrobacterium
254     tumefaciens
256 <400> SEQUENCE: 3
257  caucaucauc auggatccac caatggatct acgtctaatt ttcggtccaa c           51
259 <210> SEQ ID NO: 4
260 <211> LENGTH: 42
261 <212> TYPE: DNA
262 <213> ORGANISM: Artificial Sequence
264 <220> FEATURE:
265 <223> OTHER INFORMATION: Synthesized based on sequence from Agrobacterium
266     tumefaciens
268 <400> SEQUENCE: 4
269  cuacuacuac uagttaactc acattcgaaa tgggtggctcct tc           42
271 <210> SEQ ID NO: 5
272 <211> LENGTH: 29
273 <212> TYPE: DNA
274 <213> ORGANISM: Zea mays
276 <400> SEQUENCE: 5
277  catgccatgg cgggtggttta ttacctgct           29
279 <210> SEQ ID NO: 6
280 <211> LENGTH: 31
281 <212> TYPE: DNA
282 <213> ORGANISM: Zea mays
284 <400> SEQUENCE: 6
285  cgggatcctc atcatcagtt gaagatgtcc t           31
287 <210> SEQ ID NO: 7
288 <211> LENGTH: 5622
289 <212> TYPE: DNA
290 <213> ORGANISM: Artificial Sequence
292 <220> FEATURE:
293 <223> OTHER INFORMATION: Promoter and terminator from Zea mays as found in
294     Genbank Accession #S78780; gene from Agrobacterium
295     tumefaciens as found in Molecular and General
296     Genetics 216:388-394 (1989).
298 <400> SEQUENCE: 7
299  gctctagatt atataattta taagctaaac aacccggccc taaagcacta tcgtatcacc           60
300  tatctaaata agtcacggga gtttcgaacg tccacttcgt cgcacggaat tgcattgtttc           120
301  ttggttgaag catattcacg caatctccac acataaagggt ttatgtataa acttacattt           180
302  agctcagttt aattacagtc ttatttggat gcatatgtat ggttctcaat ccatataagt           240
303  tagagtaaaa aataagttta aattttatct taattcactc caacatatat ggatctacaa           300
304  tactcatgtg catccaaca aactacttat attgaggtga atttggtaga aattaaacta           360
305  acttacacac taagccaatc tttactatat taaagcacca gtttcaacga tcgtcccgcg           420
306  tcaatattat taaaaaactc ctacatttct ttataatcaa cccgcactct tataatctct           480

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VERIFICATION SUMMARY

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